--After one or multiple rounds of affinity selection on peptides, a subtractive or absorption step may be included to obtain phages that discriminate between two closely related peptides. For example, phages that discrimintate between the closely related peptide represented by the amino acid sequences DLVYKDPARPKI (SEQ ID NO:1) and DLVYKDPYRPKI (SEQ ID NO:2) may be obtained by affinity selection on the amino acid sequence DLVYKDPARPKI (SEQ ID NO:1), followed by absorption of phages binding to the amino acid sequence DLVYKDPYRPKI (SEQ ID NO:2). In the latter step, non-discriminative phages recognizing both peptides are removed and not used for propagation. Antibodies produced by this method can for example be used to distinguish various naturally occuring isoforms of a protein or for immunochemical assays for detecting cell transformations arising due to mutation of an oncogene or an anti-oncogene.--

Please replace the paragraph beginning at page 21, line 1, with the following rewritten paragraph:

--In the exemplary embodiment, a phagemid vector was constructed that facilitates the in vivo bacterial expression and assembly of bispecific (scFv) 2 fragments as secreted molecules or g3p fusion proteins on the surface of bacteriophages. The Fos and Jun scFv leucine zipper constructs we described (de Kruif, J., et al. J. Biol. Chem. 271, 7630 (1996); figure 3, 1 and 2) are PCR amplified using primers M13R and PDIM3 (5' -TTT GCA TTC AAG CTT TTA TTA GCC CGC ATA GTC AGG AAC ATC GTA TGG GTA TGC GGC AGC GCA ACC ACC) (SEQ ID NO:3). Primer PDIM3 replaces the Myc tag with a haemagglutinin (HA) tag and adds a stopcodon and a HindIII site to these fragments. PCR products are digested with HindIII and cloned into vector pHEN1 (Hoogenboom, H.R., et al., Nucleic Acid Res. 19, 4133 (1991)) containing a scFv gene fused to the complementary leucine zipper and a Myc tag. In the resulting constructs both scFv-zipper fragments are encoded by a single transcript. Two ribosome binding sites allow the proteins to be translated individually, the first scFv fragment fused to a Fos zipper domain and an HA tag, the second scFv to a Jun zipper and a Myc tag (Figure 3, 3). To determine the effect of the position of the scFv-zippers relative to the g3p protein, an additional construct was made in which the scFv-zipper fragments were reversed (Figure 3, 4). In suppressor E. coli strains, an amber codon inserted between the Myc tag and gene 3 permits the production of phage particles displaying a scFv fragment fused via a zipper region to gene 3. The second scFv will associate with the phage in the periplasmic space by heterodimeri zation of the Fos and Jun leucine zippers, thus creating a phage

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expressing a bispecific antibody on its surface. In non-suppressor strains, bispecific (scFv) 2 fragments linked by a Fos Jun leucine zipper will be assembled in the periplasmic space.--

Please replace the paragraph beginning at page 22, line 35, with the following rewritten paragraph:

--To test the feasability of selecting bispecific phage antibodies from a phage repertoire, bispecific phage particles from construct 4 were spiked in a 1:1000 ratio in an antibody phage display library and subjected to one round of selection in immunotubes coated with either IgG or DNP. The frequency of bispecific phages after selection was estimated by PCR on individual colonies using primers M13R and FOSCON (5'-CGC CAG GAT GAA CTC C (SEQ ID NO:4), situated in the Fos zipper). Frequencies of bispecific phages after selection were 0/32 (spiked library), 9/32 (selected on IgG) and 6/32 (selected on DNP). Calculated enrichment factors (±250x) are comparable to those obtained using monospecific phage antibodies.--

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Please replace the paragraph beginning at page 29, line 1, with the following rewritten paragraph:

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pin #	amino acid sequence		pin #	amino acid sequence	
1	MWFLTTLLLWVP	(SEQ ID NO:5)	14	KTNISHNGTYHC	(SEQ ID NO:18)
2	VDGQVDTTKAVI	(SEQ ID NO:6)	15	SGMGKHRYTSAG	(SEQ ID NO:19)
3	SLQPPWVSVFQE	(SEQ ID NO:7)	16	ISVTVKELFPAP	(SEQ ID NO:20)
4	ETVTLHCEVLHL	(SEQ ID NO:8)	17	VLNASVTSPLLE	(SEQ ID NO:21)
5	PGSSSTQWFLNG	(SEQ ID NO:9)	18	GNLVTLSCETKL	(SEQ ID NO:22)
6	TATQTSTPSYRI	(SEQ ID NO:10)	19	LLQRPGLQLYFS	(SEQ ID NO:23)
7	TSASVNDSGEYR	(SEQ ID NO:11)	20	FYMGSKTLRGRN	(SEQ ID NO:24)
8	CQRGLSGRSDPI	(SEQ ID NO:12)	21	TSSEYQILTARR	(SEQ ID NO:25)
9	QLEIHRGWLLLQ	(SEQ ID NO:13)	22	EDSGLYQCEAAT	(SEQ ID NO:26)
10	VSSRVFTEGEPL	(SEQ ID NO:14)	23	EDGNVLKRSPEL	(SEQ ID NO:27)
11	ALRCHAWKDKLV	(SEQ ID NO:15)	24	ELQVLGLQLPTP	(SEQ ID NO:28)
12	YNVLYYRNGKAF	(SEQ ID NO:16)	125	VWFHVLFYLAVG	(SEQ ID NO:29)
13	KFFHWNSNLTIL	(SEQ ID NO:17)			

Table 1. Sets of oligopeptides representing the extracellular domain of CD64.